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Maximum Match 100%
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Perfect score:
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geq
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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1788
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              MERKFMSLQPSISVSEMEPN...........KAKTKCVFPVSVWLRKETRV
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US-09-153-848-4
US-08-812-871-3
US-09-170-496D-32
PCT-US93-11153-44
US-09-170-496D-182
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US-08-513-974B-374
US-08-781-250-2
US-09-745-842-14
US-08-359-524A-4
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US-08-359-536-94-4
US-08-359-536-954-4
US-09-170-496D-78
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437 24.4 348 US-08-46-794/A-8 434 24.3 361 4 US-09-170-496D-206 434 24.3 377 4 US-09-745-842-17 424.5 23.7 374 4 US-09-745-842-15 419.5 23.5 373 3 US-08-513-9748-373 419.5 23.5 374 4 US-09-102-710B-3 419.5 23.3 375 1 US-08-442-134A-2 416 23.3 375 1 US-08-444-281B-2 416 23.3 375 1 US-08-444-281B-2 416 23.3 375 1 US-08-444-581B-2 416 23.3 375 1 US-08-444-134A-3 416 23.3 375 2 US-08-447-194A-3 416 23.3 375 2 US-08-749-707-3 416 23.3 375 2 US-08-98-79-707-3 416 23.3 375 2 US-08-79-922-3 406.5 22.7 398 1 US-09-947-922-3 406.5 22.7 398 1 US-08-097-938-6 406.5 22.7 398 1 US-08-097-938-6 406.5 22.7 398 1 US-08-097-938-6 406.5 22.7 398 1 US-08-476-976-6	45	44	43	42	41	40	39	38	37	36	35	34	33	32	<u>3</u> 1	30	29	28
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ALIGNMENTS

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Sequence 2, Application US/09585876

Retent No. 6586205

REMERAL INFORMATION:

APPLICANT: Glucksmann, Maria Alexandra

APPLICANT: Silos-Santiago, Immaculada

ITITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and

TITLE OF INVENTION: USes Thereof

FILE REFERENCE: 5800-88

CURRENT APPLICATION NUMBER: US/09/585,876

CURRENT FILING DATE: 2000-06-01

EARLIER APPLICATION NUMBER: 60/182,061

EARLIER FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO

LENGTH: 346

TYPE: PRT

ORGANISM: Homo sapiens

US-09-585-876-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 344; Conservative
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                                                                                                                                                                                                                                                             NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSBQ
NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                         SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                                   NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                                                                                                                          NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                                                                                                                                                                                      NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPUTER: DOS
CORRATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,
APPLICATION NUMBER: MARCH 19, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,79
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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APPLICANT:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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Local Similarity 38.0%;
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CITY: King of Prussia
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PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 317
                                                     HYVSLFVGFIIPEVIIIVCYTMILTTLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSEM
                                                                                          NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 261
                                                                                                                              QNINLVTQKKARFYCVGIWIFVILTSSPFLMAKPQKDGKNNTKCFEPPPQDNQTKNHVLVL
                                                                                                                                                                   RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 201
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HALSEY, WENDY
ELLIS, CATHERINE
AMES, ROBERT
                                                                                                                                                                                                                                                                                                                                                           Conservative
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FastSEQ for Windows Version
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SARAU, HENRY
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US-08-153-848-44

Sequence 44, Application US/08153848 Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Godiska, Ronald Gray, Patrick W. Schweikart, Vicki RESULT 4

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TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RE(
FILE REFERENCE: GH-70001-1D1
CURRENT APPLICATION NUMBER: US/09/586,924
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR APPLICATION NUMBER: 08/844,795
PRIOR APPLICATION NUMBER: 08/844,795
PRIOR APPLICATION NUMBER: 08/844,795
PRIOR FILING DATE: 1997-04-22
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US-09-586-924-2
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SEQ ID NO 2
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Patent No. 650687
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ORGANISM: HOMO SAPIENS
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                                                                                                                        262
                                                                                                                                                                                                                                            130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDGKNNTKCFEPPQDNQTKNHVLVL
                                                                                                                                                                                                                                                                                   145 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 201
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                                                                                                                                                                                                                                                                                                                                                                   85 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVRFLAMVHPF 144
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                                                                                                           PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 317
                                                                                                                                                                                               NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 261
                                        SALRK 322
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STERK 311
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HALSEY, WENDY
BILIS, CATHERINE E.
AMES, ROBERT S.
FOLEY, JAMES J.
SARAU, HENRY M.
CHAMBERS, JON
                                                                                 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDFLLYFFSGGNFRKRL-
                                                                                                                                                                                                                                                                                                                            LICVCTLPIRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFEMTAMSFFRCIAIVFPV 129
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RESULT 5
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153.845
PILING DATE:
CLASSIPTION
Sequence 3, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.0%; Score 483.5; DB 1; Length 329; Best Local Similarity 34.6%; Pred. No. 2.9e-30; Matches 115; Conservative 63; Mismatches 129; Indels 25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
PILLING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greea E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31794
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 339 amino aci
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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                                                                                                                                                            MYPFVAEKFRHALCNLLCGKRLKGPPPSFEGK 327
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    RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/8:
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Muzong Chen
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
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                                                                                                                   304 LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
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                                                                                                                                                                                TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPL 303
                                                                                                                                                                                                                                                                          NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALT 247
                                                                                                                                                                                                                                                                                                                  ISADRFLAIVHPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ- 183
                                                                                                                                                                                                                                                                                                                                           LSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSBQNGSVTSCLEL 190
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                                                                                 MYFFVAEKFRHALCNLLCGKRLKGPPPSFEGK 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 amino acids
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Best Local Similarity
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
PILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gray, Patrick W. APPLICANT: Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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: Illinois
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                                                                                                                                                                                                                                                                                                     EVAPPGLITNESLATAEQCGQETPLENMLEASFYLLDFILALVGNTLALWLFIRDHKSGT
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TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPL 303
                                                                           -LYR-EKASHHALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
                                                                                                                                                                                                                                                                SVNVFMLNIAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTV 131
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6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (312) 474-0448
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                                                                                                                                                                                                                                                                                                                                                                           27.0%; Score 483.5; DB 3; Length 339; 34.6%; Pred. No. 2.9e-30; tive 63; Mismatches 129; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 6107475el Seven Transmembrane Receptors
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TYPE: amino acid;
; TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
APPLICATION NUMBER: US 07/977,452
                                                                                                                                                                                                                                                                                                                         / Match 27.0%; Score 483.5; DB 3; Local Similarity 34.6%; Pred. No. 2.9e-30; les 115; Conservative 63; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Godiska, Ronald
191 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR----KALT
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                                                              LSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLEL
                                                                                                                                                     PANVFLMHLAVADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTC
                                                                                                                                                                                             SVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTV 131
                                                                                                                                                                                                                                                                                 EMEPNG---TFSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKST 71
                                                                                                                                                                                                                                         EVAPPGLITNESLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 339 amino acids
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TELEFAX: (312) 474-0448
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CITY: Chicago
STATE: Illinois
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ZIP: 60606
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Schweikart, Vicki L.
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RESULT 9
PCT-U993-11153-44

/ Sequence 44, Application PC/TUS9311153
/ GENERAL INFORMATION:

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; ORGANISM: Homo sapiens
US-09-170-496D-32
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Best Local Similarity
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SEQ ID NO 32
LENGTH: 339
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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REPERENCE: AREN-0040
CURRENT APPLICATION UMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                   APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OP INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
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                                                                                                                                                                                                                                                                                                                                   304 LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
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                                                                                                                                                                                                                                                                                            MYFFVAEKFRHALCNLLCGKRLKGPPPSFEGK 327
                                                                                                                                                                                                                                                                                                                                                                              MIAIVLAIFLVCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCI,TSLNGALDPI
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Marshall, O'Toole, Gerstein, Bicknell
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Pred. No. 2.9e-30;
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PCT-US95-07180-2
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                                    Sequence 2, Application PC/TUS9507180
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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LENGTH: 339 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER: US 0.
PILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                     CORRESPONDENCE ADDRESS
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CITY: CI
STATE:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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                                                                                                                                                                                                                                                                         296
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                                                                                                                                                                                                                                                                                                                                                                                                                                           184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 PANVFLMHLAVADLSCVLVLPTRLVYHPSGNHWPFGEIACRLTGFLFYLNMYASIYFLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 SVNVFMLNLAISDLLFISTLFFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTV 131
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                                                                                                                                                                                                                                                                                                                                                                                               TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                           -LYR-EKASHHALVSLAVAFTFPFTTTVTCYLLTIRSL-----RQGLRVEKRLKTKAVR
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  CARELLA, BYRNE,
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    BAIN, GILFILLAN, CECCHI,
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Cc
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                     RESULT 11
US-09-170-496D-182
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                                                                                                                                                                                Sequence 182, Application US/09170496D Patent No. 6555339 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
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TYPE: amino acids
TOPOLOGY: line
(OLECTION)
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CURRENT APPLICATION DATA:
APPLICATION UNMERS: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 07068
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STREET: 6 BECKER FARM ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 LSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEONGSVTSCLEL 190
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34.6%; Pred. No. 2.9e-30;
tive 63; Mismatches 129
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                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 5.36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
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SEQ ID NO 182
LENGTH: 339
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TYPE: PRT
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 ISADRFLAIVHEVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ- 183
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). 6114139
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Fujii, Ryo
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RESULT 13
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FILING DATE: 30-8EP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
DATA:
PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
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PILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 45
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                                                                                                                                                                                          195
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                                                                307
                                                                                                                                                                                                                                                                                   134 VVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSE()NGSVTSCLE- 189
                                                                                          299 CFNPLLYYFAGENFKDRLKSALRK 322
                                                                                                                                                                                                                                                                                                                   76 SVYMENLALADELYVLTLDALIEYYENKTDWIFGDVMCKLOREIEHVNLYGSILELTCIS
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Similarity 30.6%;
99; Conservative 82
                                                                                                                                                                                        TADEYLRSYFVYSMCTTVFMFCI----PFIVILGCYGLIVKALIYKDLDNSPLR---RK
                                                                                                                                                       ALTTIIITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANA 298
                                                                                                                                                                                                                 -----LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRK 244
                                                              CVDPILYFLAGDTFRRRLSRATRK 330
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                                                                                                                           STYLVIIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNS
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Pred. No. 1e-28;
2; Mismatches 117;
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; Patent No. 6010877
; GENERAL INFORMATION:
; APPLICANT: Sathe, (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Matches
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TOPOLOGY: lir
MOLECULE TYPE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Bergi
APPLICANT: Mao,
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linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acid
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
TO //8/781 250
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CORRESPONDENCE ADDRESS:
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CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 447.5; DB 3; sal Similarity 31.6%; Pred. No. 2e-27; 109; Conservative 74; Mismatches 141;
                                                                                                                                                                                                     180 NVNNATTTCFEGFSKRVWKTYLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLS
                                                                                                                                                                                                                                                                                                                                                        120 VMMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIML-LDSGS
                                                                                                                                                                                                                                                                                                                                                                                                           61 LEVECERMINARSETATETTHLAVSDLLEVCTLEEKT-EYNENRHWEFGDTLCKISGTAFL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 IYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLY 119
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                                                                                                                                                                                                                                                                                                        TNIYGSMLFLTCISVDRFLAIVYPFRSRTIRTRRNSAIVCAGVWILVLSGGISASLFSTT
                                                  LAAANACFNPLLYYFAGENFKD-----RLKSALRKGHPQKAK 329
                                                                                                     QIGTNKKKVLKMİTVHMAVFVVCFVPYNSVLFLYALVRSQAITNCFLERFAKIMYPİTLC
                                                                                                                                                GLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCK---DRLHKALV-ITLA
                                                                                                                                                                                                                                           EQNGSVTSCLELNLYKIAK--LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRRFIDFOFODSNSSLRPRLGNATANNT--CIVDDSFKYNLNGAVYSVVFILGLITNSVS
LATLNCCFDPFIYYFTLESFQKSFYINAHIRMESLFKTETPLTTK 343
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Bergsma, Derk
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RESULT 15
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US-09-745-842-14
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SEQ ID NO 14
LENGTH: 373
TYPE: PRT
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Patent No. 5871963
GENERAL INFORMATION:
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Best Local Similarity
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FILE REFERENCE: 44481-5053-US
FURRENT APPLICATION NUMBER: US/09/745,842
CURRENT FILING DATE: 2000-12-26
CURRENT FILING DATE: US. 60/171,622
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STREET: 1800 ... STREET: Washington STATE: D.C. COUNTRY: USA ZIP: 20036-5869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hollopeter, Gunter APPLICANT: COR Therapeutics, Inc. TITLE OF INVENTION: P2712 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                           APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                        ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP STREET: 1800 M Street, N.W.
                                                                                                                                                                                                                                                                                                                                                            324
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ANT: Conley, Pamela B.
ANT: Jantzen, Hans-Michael
ANT: Ramakrishnan-DuBridge, Vanitha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 RSYFIYSMCT----TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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TOPOLOGY: li
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                                                                  336 SRATRK 341
                                317 KSALRK 322
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amino acid
                                                                                                   YHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANACENPLLYYFAGENEKDRL 316
                                                                                                                                           --TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVIIVLTVFAVSYIP 275
                                                                                                                                                                              YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPBSGLRVSHRKALTTIIITLIIFFLCFLP 262
                                                                                                                                                                                                                  KKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTIT-CYDTTSDEYLRSYFIYSMCT--
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Search completed: March 18, 2005, 16:22:32 Job time: 33.2456 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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442
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447.5
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seq length:
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Match
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1: pir1:*
2: pir2:*
3: pir3:*
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           MERKFMSLQPSISVSEMEPN......KAKTKCVFPVSVWLRKITRV 346
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S43252
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T09508
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I49339
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JC4162
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angiotensin recept platelet-activatin chemokine (C-C) re proteinase activat macrophage inflamm G protein-coupled probable chemoattr G protein-coupled lymphocyte-specifi G protein-coupled MIP-1 alpha recept somatostatin recept somatostatin recept g protein-coupled MIP-1 alpha rocept somatostatin recept som
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S337/3

G protein-coupled receptor - chicken

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S33733

R;Rebb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstoch

R;Rebb, T.S.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstoch

R;Rebs, Lett. 324, 219-225, 1993

A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.

A;Reference number: S33733; MUID:93285340; PMID:8508924

A;Accession: S33733; MUID:93285340; PMID:8508924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g39508
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
  heptahelical P2Y5-like receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
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ALIGNMENTS

Matches 99; Conser	99; Conservative 84; Mismatches 115; Indels 26; Gaps
Ş	ENFKREFFPIVYLIIFFWGVLGN
망	16 ELLAGGWAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWHFVFHMRPWSGI 75
γQ	74 NVFMLNLAISDLLEISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLS 133
Db	76 SVYMENIALADELYVITLEBALIEYYENKTDWIEGDVMCKLQREIEHVNLYGSILELTCIS 135
Ş	134 VVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLE- 189
В	136 VHRYTGVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTIT-CYDT 194
8	
뮹	195 TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDNSPLRRK 246
Ş	,TTWKVGLCKI
뭥	247 SIYLVIIVLTVEAVSYLPEHVMKTLNLRARLDEQTPQMCAENDKVYATYQVTRGLASLNS 306
Ş	299 CENPLLYYFAGENFKDRLKSALRK 322
망	307 CVDPILYFLAGDTFRRRLSRATRK 330

```
G protein-coupled receptor 6H1 - chicken
N,Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50241; JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T ce
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:;
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Accession: JC4618
A:Molecule type: TC4618; MUID:96190677; PMID:8619790
A:Molecule type: TC4618; MUID:96190677; PMID:8619790
F;89-109/Domain:
          C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane protein
E;15-40/Domain: transmembrane #status predicted <TM2>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;51-74/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383;
A;Experimental source: T-cells
                                                                                                                                  A;Gene: p2Y5
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R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely
A;Reference number: JC5549; MUID:97366605; PMID:9223435
A;Accession: JC5549
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A; Residues: 1-370 < JAN>
                                                                                                                                                                            Comment: This
                                                                                                                                                           Genetics:
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Pred. No. 4.2e-29;
'4; Mismatches 141;
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       predicted
                                                                                                                                                                       T-cell
                                                                                                                                                                                                                     PIDN:AAB06587.1;
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  A;Map position: 3pter-3qter (;Superfamily: ATP receptor Pau C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #;52-77/Domain: transmembrane #status predicted <TML> F;88-111/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                   A/Status: preliminary
A,Molecule type: mrNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:249205;
C;Comment: This receptor belongs
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA970; A;Experimental source: erythro leukemia cells R;Leon, C.; Vial, C.; Cazenave, J.; Gaychet, C.; submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor A;Reference number: S54253
                                                                                                                                  A;Cross-references: GDB:677125; OMIM:601167
                                                                                                                                                           A;Gene: p2Y1; GDB:P2RY1
                                                                                                                                                                                                                                                                                                                              A; Accession: S54253
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R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A;Title: Cloning and chromosomal localization of the human A;Reference number: JC4615; MUID:96158962; PMID:8579591
                                                                                                                                                       Affither Cloning and tissue distribution of the human P2Y1 receptor.
                                                                                                                                                                                                                                                                                      JC4737
G prot
A; Accession: JC4615
                                                                                            A; Molecule type: DNA
A; Residues: 1-373 <JAN>
                                                                                                                                  A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
                                                                              A; Cross-references: UNIPROT: P47900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQNNTEQRTCFE-NFPESTWKTYLSR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHVTSIRSAWILCGIIWILIMASSI----MLLDSGSEQNGSVTSCLELNLYKIAKLQTMNY 203
                                                                                                                                                                                                                                                                                                                                                                      VPYNITLILYSLMRT---OTWINCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSD
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Pred. No. 3.9e-29;
                                                          GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g18394:
hu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 119;
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<TM6>
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                            purinoceptor
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A; Molecule type: mRNA A; Residues: 1-373 < AYY>

;Genetics:

NID:g798835; PIDN:CAA89066.1; PID:g798836 to a family of G protein-coupled receptor

receptors.

It responds

prote

PIDN:AAA97872.1;

PID:g1147731

transmembrane

#status

predicted <TM3>

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P2Y receptor - bovine
C,Bpecies: Bos primigenius taurus (cattle)
C,Bpecies: Bos primigenius taurus (cattle)
C,Bete: 12-Oct-1955 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: JC4162
R;Henderson, D.J; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Title: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1.373 <HEN>
A;Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g103
A;Experimental source: sortic endothelial cell
C;Genetics:
C;Koywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
C;Koywords: glycoprotein; transmembrane #status predicted <TM1>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;124-150/Domain: transmembrane #status predicted <TM5>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;214-238/Domain: transmembrane #status predicted <TM5>
F;211-27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;355-9/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;361-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;111,27,113,197/Binding site: carbohydrate (Asn) (covalent) (by protein kinase A) #status predict F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predict F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C and calmodulin-dependent)
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                                                                            24.7%;
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                                                          Score 442; DB 2;
Pred. No. 1.2e-28;
8; Mismatches 109;
                                                                                            Length 373
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                            24;
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    RESULT
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R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyt A;Reference number: A45680; MUID:93188173; PMID:8383238
A;Accession: B45680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
845680
G protein-coupled peptide receptor EBI 2 - human
G proteis: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B45680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127096, |
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-361 <BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P32249; GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057
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Best Local (
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308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 24.6%; Score 440; DB 2; I
Similarity 32.1%; Pred. No. 1.7e-28;
02; Conservative 63; Mismatches 135;
                                                                                                                                            TLIIFFLCFLPYHTLRTVHLTTWKVGL-----CKDR--LHKALVITLALAAANACFNPLL 304
                                                                                                                                                                                                                                            KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE-----VPESGLRVSHRKALTTIII
                                                                                                                                                                                                                                                                                                                                          AMVHPFRLLHVTSIRSAWILCGIIWILIMASSI-MLLDSGSEQNGSVTSCLEL-NLYKIA 196
                                                                                                                                                                                                                                                                                                                                                                                             NLVÍSDILFTTALÞTRIAYÝAMGFDWRIGDALCRÍTALVFÝINTÝAGVNFMTCLSIDRFI
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     YFFACKGYKRKVMRMLKR
                                                YYFAGENFKDRLKSALRK
                                                                                              IIVVFVLCFTPYHVAIIQHMIK-KLRFSNFLECSQRHSFQISLHFTVCLMNFNCCMDPFI
                                                                                                                                                                                            SLPWILLGACFIGYVLPLIIILICYSQICCKLFRTAKQNPLTEKSGV----NKKALNTIIL
                                                                                                                                                                                                                                                                                             AVVHPLRYNKIKRIEHAKGVCIFVWILVFAQTLPLLINPMSKQEABRITCMEYPNFESTK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNGTFSNMNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML
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PMID:8383238
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R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D. Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression clonding of an ATP receptor from mouse neuroblastoma A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-373 <LUSA
A;Cross-references: UNIPROT:P35383; GB:L14751; NID:g309457; PIDN:AAA39871.1;
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein
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A;Molecule type: mRNA
A;Mol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP receptor P2u - mouse
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C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Mus musculus (house mouse);Date: 13-Jan-1995 #text_change;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                               Matches
                                                                                                                      Query Match
Best Local Similarity
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Best Local
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98; Conservative
                                        SEMEP----
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                                                                                         23.6%; ilarity 31.6%; Conservative 6
  -NGTFSNNN-SRNCTI-ENFKREFFFIVYLIIFFWGVLGNGLSIYVFLQPY 67
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                                                                                         Score 421.5; I
Pred.'No. 5.6e-
59; Mismatches
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Pred. No. 3.4e-28;
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                                                                                                                   .6e-27;
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RESULT 10
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P-2U nucleotide receptor -
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R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Se Nature 349, 342-346, 1991
A;Title: Cloning by functional expression of platelet-activating A;Reference number: S13638; MUID:91101726; PMID:1846231
A;Accession: S13638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P21556; GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443 A;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, releas: C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         platelet-activating factor receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13638
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S13638
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A; Residues: 1-342 < HON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                             RLLHVTSIRSAWILCGIIWILIM--ASSIMLLD----SGSEQNGSVTSCLELNLYKIAK 197
                                                                                                                                                    LCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPLLYYFAGENFK 313
                                                   DRLKSALRKGHPQKAKTKC 332
                                                                                                                                                                                                                                                      LQTWNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSSSRVDSEFRYTLFPIVYSIIFVLGIIANGYVLMVFARLYPSKKLNBIKIFMVNLTVAD
  KHLSEKL-:
                                                                                                                                                                                                        PVLIIHICIVLGFFIVFLLILFCNLVIIHTLLRQPVKQQRNAEVRRALWMVCTVLAVFV 242
                                                                                                                                                                                                                                                                                                            KTAQATTRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNKAGSGNITRCFE-HYEKGSK 182
                                                                                                                                                                                                                                                                                                                                                                                                                LLFLITLPLWIVYYSNQGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVNVFMLNLAISD 84
                                                                                                      ICFVPHHMVQ-LPWTLAELGMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANACENPLLYYFAGENFKDRLKSALRKGHPQKAKT
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  -NIMRSSOKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado,
317
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platelet-activating factor receptor - human
C;Bpccies: Homo sapiens (man)
C;Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text_change 09-Jul-2004
C;Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text_change 09-Jul-2004
C;Accession: A40191; JH0479; A41079; JC1359; A42831; I51923
R;Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A;Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, c
A;Reference number: A40191; MUID:9250505; PMID:1374385
A;Reference number: A40191; MUID:9250505; PMID:1374385
A;Accession: A40191
A;Accession: A40191
A;Cross-references: UNIPROT:P25105; GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:
A;Cross-references: UNIPROT:P25105; GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A;Title: Characterization of a human cDNA that encodes a functional receptor for
A;Reference number: JH0479; MUID:92028922; PMID:1658963
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A, Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic A, Accession: A54946; MUID:94211846; PMID:8159738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
A40191
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C;Superfamily: ATP receptor P2u
C;Keywords: G protein -----
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A/Note: parts of this sequence were
C/Genetics:
                                                                       A, Molecule type: mRNA
A, Residues: 1-342 < YER>
                                                                                                                        A; Accession: JH0479
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,Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
;Experimental source: granulocyte, cell line HL-60 all
;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local &
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;Date: 11-Nov-1994 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 23.3%; Score 416; DB 2; Local Similarity 31.6%; Pred. No. 1.6e-26;
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A;Note: the authors translated the codon AAT for residue 316 R;Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992
A;Title: The human platelet-activating factor receptor gene (A;Reference number: A42831; MUID:92347886; PMID:1322356
A;Accession: A42831
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A;Title: Molecular cloning and characterization of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activating factor receptomarkers of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of the platelet-activation of th
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F;184-205/Domain: transmembrane #status predicted <TRV-
F;233-253/Domain: transmembrane #status predicted <TVIV-
F;277-297/Domain: transmembrane #status predicted <VIII-
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A;Residues: 1-226,'TG',229-342 <SEY>
A;Residues: 1-226,'TG',229-342 <SEY>
A;Residues: 1-226,'TG', NID:g190697; PIDN:AAA60214.1; PID:g190698
A;Cobe: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R;Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for an A;Reference number: I51923, MUID:93192035; PMID:8383507
A;Accession: I51923
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C; Superfamily: ATP receptor P2u
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Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating
A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079
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A,Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581
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A; Residues: 1-315,'N',317-342 < SUG>
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MVCTVLAVFIICFVPHHVVQ-LPWTLAELGFQDSKFHQAINDAHQVTLCLLSTNCVLDPV
                                                                                                                                                TIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPL
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platelet activating factor receptor - mouse (Species: Mus musculus (house mouse) (?Species: Mus musculus (house mouse) (?pate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 (?Accession: $63666 R;Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shim: Blochem. J. 314, 671-678, 1996 R;Ishie. J. 314, 671-678, 1996 A;Title: A murine platelet-activating factor receptor gene: cloning, chromose, A;Reference number: $63666; MUID:96239129; PMID:8670084 A;Accession: $63666
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A; Residues: 1-341 <ISH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51667
C;Accession: I51667
R;Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.
Nature 368, 648-651, 1994
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Matches
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;Residues: 1-420 <GE
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Xenopus laevis (African clawed frog)
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MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTQKIPRLDITTCHDVLDLKDLKDFYIYYFSSF--CLLFFFVPFIITTICYIGIIRSLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LALAAANACFNPLLYYFAGENFKDRLKSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ---NGSVTSCLELNLYKIAKLQTMNYIALVVGCLL----PFFTLSICYLLIIRVLLK 230
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                                                       Score 404; DB 2;
Pred. No. 1.4e-25;
6; Mismatches 134
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1.2e-25;
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                                                                                                                                                NID:g1256924;
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A;Molecule type: mRNA
A;Residues: 1-137,'A','139-397 <BOE>
A;Residues: 1-137,'A','139-397 <BOE>
A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
A;Note: the authors translated the codon GTC for residue 68 as Ile and AAC fo
R;Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
                                                                                                                                                                                                                                                              C;Superfamily: ATP receptor P2u
C;Superfamily: ATP receptor P2u
F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status predicted
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C; Superfamily: z
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A;Title: Molecular cloning, expression and potential functions of the human prot A;Reference number: S64709; MUID:96177879; PMID:8615752
A;Accession: S64709
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A; Residues: 29-397 <1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteinase-activated receptor 2 precursor - human C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S66518; S64709; G02131
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A; Accession: G02131
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100 RGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGS-----EQNGSVTSC
                                                      77
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                                                                                                                                                                                            Similarity
                                                      FLPIVYTIVFVVGLPSNGMALWVFLFRTKKKHPAVIYMANLALADLLSVIWFPLKIAYHI 136
                                                                                                         FFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYL 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVIYCFLTKKFRKHLS---EKFYSMRSSRKC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLLYYFAGENFKDRLKSALRKGHPQKAKTKC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEHYEPYSVPILVVHVFIAF---CFFLVFFLIFYCNLVIIHTLLTQPMRQQRKAGVKRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LE-LNLYKIAKLQTMNYIALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKA
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                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: U36753; NID: g1208539; PIDN: AAA90957.1;
                                                                                                                                                                                       22.4%;
                                                                                                                                                                   69;
                                                                                                                                                             Score 400.5; DB 2;
Pred. No. 3.1e-25;
59; Mismatches 121;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                   Length
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A.; Kahn,
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angiotensin receptor homolog APJ - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004 (C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004 (C;Daccession: 138435 (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroperature) (Petroper
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I38435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Map position: 11q12
A/Introns: #status absent
C/Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Rosidues: 1-380 <RES>
A;Cross-references: UNIPROT:P35414; EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g4253
Search completed: March 18,
Job time : 28.1272 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.3%; Score 398; DB 2; Length 380; Best Local Similarity 29.2%; Pred. No. 4.7e-25; Matches 100; Conservative 71; Mismatches 134; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
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                                                                                                                                                                                                                                                                                                         239 ---GLR-KRRELISIIVVLVVTFALCMMPYHLVKTLYMLGSLLHWP----CDFDLFLMNIF 291
                                                                                                                                                                                                                                                                                                                                                                                   234 PESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVH----LTTWKVGLCKDRLHKALVI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 CLELNLYKIAKLQT------MNYIALVVGCLLPFFTLSICYLLIIRVLL------KVEV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 TVLSVVRFLAMVHPPRLLHVTSIRSAWILCGIIWIL--IMASSIMLL-DSGSEQNGSVTS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 - CRSVRTVKQMQVSLTSKKHSR 381
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                                                                                                                                                                                                                            290 --TLALAAANACENPLLYYEAGENEKDRIKSAIRKGHPQKAKT 330
                                                                                                                                                      292 PYCTCISYVNSCLNPFLYAPFDPRPRQACTSMLCCGQSRCAGT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RRSADIFIASLÁVADLTFVVTLPLWÁTYTYRDYDWPFGTFFCKLSSYLIFVNMYASVFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSVNVFMLNLAISDLLFISTLFFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLAIGVFLFPAFLTASAYVLMIRMLRSSAMDENSEK-KRKRAIKLIVTVLAMYLICFTPS 303
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-585-876-1
US-09-044-404A-1
US-09-586-924-1
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US-09-115-848-43
US-09-015-843A-43
US-09-088-337B-43
PCT-US95-07180-1
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US-08-476-000-62
US-08-476-160-62
US-08-486-673B-62
US-08-486-673B-62
US-08-889-108-16
PCT-US94-10358-16
US-08-889-108-16
PCT-US94-10358-16
US-08-454-549-1
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US-09-016-434-1259	US-09-170-496D-221	US-09-170-496D-107	US-09-364-425B-26	US-08-724-974A-1	US-09-170-496D-117	US-08-676-351-1	US-09-170-496D-225	US-09-054-272-1	US-09-023-655-1186	US-09-016-434-1239	US-09-048-916B-3	US-09-510-473-3	US-09-170-331-3	US-08-514-451A-3	US-08-553-058C-3	US-08-911-245-3	US-08-149-093A-3
Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence
1259, Ap	221, App	107, App	26, Appl	1, Appli	117, App	1, Appli	225, App	1, Appli	1186, Ap	1239, Ap	3, Appli	3, Appli	3, Appli	3, Appli	3, Appli	3, Appli	3, Appli

ALIGNMENTS

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)
US-09-585-876-1
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APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 5800-88

CURRENT APPLICATION NUMBER: US/09/585,876
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER FILING DATE: 2000-02-11
NUMBER: FILING DATE: 2001-02-11
NUMBER: FILING DATE: 2001-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
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Best Local
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TYPE: DNA
ORGANISM: Homo
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Similarity 99.8%;
39; Conservative
                                                                    GCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA
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GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC
                                         GCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCCTTCAGGGCTGACTATTATCTTAGA
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GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: ELLIS, CATHERINE
APPLICANT: AMES, ROBERT
APPLICANT: AMES, ROBERT
APPLICANT: SARAU, HENRY
TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 790 Swedeland Road, P.O. Box 1539
                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-044-404A-1
                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09044404A Patent No. 6200775
STATE: PA
COUNTRY: US
ZIP: 19406
                                                     CITY: King of Prussia
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SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.9%;
Best Local Similarity 51.5%;
Matches 451; Conservative
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APPLICATION DATE: 08/844,795
PILING DATE: APRIL 22, 1997
ATTORNEY/ACENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-70001-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/99/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
DEFFOR NATE: TASSIFICATION A
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatit
OPERATING SYSTEM: DOS
COPPERATING SYSTEM: DOS
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                 TGGCTTTATCATCCCTTTTGTTATTATATTGTCTGTTACACAATGATCATTTTGACCTT
                                                                                                                              GAATCTCTATAAAATTGCTAAGCTGCA-----GACCATGAACTATATTGCCTTGGTGGT 623
                                                                                                                                                                                                        AATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCT
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Pred. No. 1.6e-35;
0; Mismatches 398;
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; SOPTWARE: FABTSEQ for Wi
; SEQ ID NO 1
; LENGTH: 1578
; TYPE: DNA
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-586-924-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHAMBERS, JON
APPLICANT: CHAMBERS, JON
TITLE OF INVENTION: CDNA CLONE HMTMP81 THAT ENCODES A NOVEL
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
FILE REFERENCE: GH-70001-1D1
CURRENT APPLICATION NUMBER: US/09/586,924
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR FILING DATE: 1998-03-19
PRIOR PRICHATION NUMBER: 08/044,795
PRIOR APPLICATION NUMBER: 08/044,795
PRIOR FILING DATE: 1997-04-22
JUNDBER OF SEQ ID NOS: 2
JUNDBER OF SEQ ID NOS: 2
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US-09-586-924-1
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APPLICANT: SATHE,
APPLICANT: HALSEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09586924
Patent No. 6506878
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.9%; Score 145.2; DB 4; Length 1578; Best Local Similarity 51.5%; Pred. No. 1.6e-35; Matches 451; Conservative 0; Mismatches 398; Indels 27;
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HALSEY, WENDY
ELLIS, CATHERINE E.
AMES, ROBERT S.
FOLEY, JAMES J.
SARAU, HENRY M.
CHAMBERS, JON
                                                                                                     TCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTG
                                                                                                                                                         ATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCT
                                                                                                                                                                                                                                        AGGCTTCTTTGGCAATGGCTTTGTGCTCTATGTCCTCATAAAAACCTATCACAAGAAGTC
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                                   ATATTTCTTTCTGGGGGTAACTTTAGGAAAAGGCT
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CCGCCTCAGCACCTATGCTTTGTATGTCAACCTCTATTGTAGCATCTTCTTTATGACAGC
                                                                          GCCTCTCCGTGTGGTCTATTATGTCCACAAAGGCATTTGGCTCTTTGGTGACTTCTTGTG
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TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G ITILE OF INVENTION: Receptors FILE REFERENCE: AREN-0040 CURRENT APPLICATION UNMBER: US/09/170,496D CURRENT FILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 294 SOFTWARE: Patentin version 3.1 SEQ ID NO 31 SEQ ID NO 31 SEQ ID NO 31 TYPE: DNA ORGANISM: Homo sapiens US-09-170-496D-31
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US-09-170-496D-31
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GENERAL INFORMATION:
                                                                                                                    Query Match 9.5%;
Best Local Similarity 48.8%;
Matches 339; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
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                                                   GAAGTCCGTGGTCATAACCTTGTCTCTGGCTGCATCCAATTGTTGCTTTGACCCCTCTCCT 1347
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                                                                                                                      Score 99.4; DB 4;
Pred. No. 5.3e-21;
0; Mismatches 341;
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RESULT 5
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Patent No. 6500938
GENERAL INFORMATION:
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
1490
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/016,434
FTILING NAME:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                       FILING DATE:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: ::
SEQUENCE CHARACTERISTICS:
LENGTH: 1900 base pairs
TYPE: nucleic acid
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LIBRARY: GENBA
CLONE: 9992699
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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REGISTRATION NUMBER: 37,071
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Pred. No. 8e-21;
0; Mismatches 341;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             Matches 339;
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APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
PILING DATE: 17-NOV-1992
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 111
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ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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TGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTG 478
                              TCAACATGTACGCCAGCATCTACTTCCTCACCTGCATCAGCGCCGACCGTTTCCTGGCCA 1097
                                                                                                 TGGCCGTGGCCGACTTGTCGTGCGTGCTGGTCCTGCCCACCCGGCTGGTCTACCACTTCT
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Pred. No. 8e
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/299,843A
                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            FILING DATE: 01-JUN-1998
PRIOR APPLICATION UMER: US 08/153,848
FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
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    Application US/09299843A
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                                        474-0448
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US-09-299-843A-43
                                                                   Sequence 43, Applicati
Patent No. 6348574
GENERAL INFORMATION:
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Best Local Similarity 48.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
VOLFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                                                                                                                                         1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858 TGTGGCTTTTCATCCGAGACCACAAGTCCGGGACCCCGGCCAACGTGTTCCTGATGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 TATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          798 TGTTCGCCTCCTTCTACCTTCTGGATTTTATCCTGGCTTTAGTTGGCAATACCCTGGCTC 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 TTTTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAACATGTACGCCAGCATCTACTTCCTCACCTGCATCAGCGCCGACCGTTTCCTGGCCA 1097
                                                                                                                                                                                       TCGTGCCCTACCACGTCAACCGCTCCGTCTACGTG 1477
                                                                                                                                                                                                        TCCTGCCCTATCACACACTGAGGACCGTCCACTTG 813
                                                                                                                                                                                                                                                                                                                                                GTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGG 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGGAACCACTGGCCATTTGGGGAAATCGCATGCCGTCTCACCGGCTTCCTCTTCTACC 1037
                                                                                                                                                                                                                                                                                                                       GCTACCTGCTGATCATCCGCAGCCTGCGGCAGGCCCTGCGTGTGGAGAAGCGCCTCAAG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCCGTGGCCGACTTGTCGTGCGTGCTGGTCCTGCCCACCCGCCTGGTCTACCACTTCT
                                                                                                                                                                                                                                                                                      TTTCTCACAGGAAGGCACTGACCACCATCATCACCCTTGATCATCTTCTTCTTGTGTT
                                                                                                                                                                                                                                                                                                                                                                                      CCCTGG-----TGTCCCTGGCAGTGGCCTTCACCTTCCCGTTCATCACCACGGTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                       CCATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCCATTTTTCACACTCAGCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTTCCTGTGGGTGGTGGCTGTGGCCATGGCCCCGCTGCTGGTGAGCCCACAGACCG 1217
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                                                                                                       Application US/09088337B
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701..1717
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                                                                                                                                                                                                                                                       - ACCAAGGCAGTGCGCATGATCGCCATAGTGCTGGCCATCTTCCTGGTCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1901;
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-088-337B-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <a href="https://doi.org/liber.108/18/10-20m.1998">URKNOWN></a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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LENGTH: 1901 base pairs
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall,
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                                                                                                                                                                                                                                  CTGGGAACCACTGGCCATTTGGGGAAATCGCATGCCGTCTCACCGGCTTCCTCCTTCTACC 1037
GGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGC 538
                                                                                                                                                                                                                                                                       GAGGCTCCAATTGGATATTTGGAGACCTGGGCCTGCAGGATTATGTCTTATTCCTTGTATG 358
                                           TTGTGCACCCGGTCAAGTCCCTCAAGCTCCGCAGGCCCCTCTACGCACACCTGGCCTGTG
                                                                                       TEGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTG 478
                                                                                                                                          TCAACATGTACGCCAGCATCTACTTCCTCACCTGCATCAGCGCCGACCGTTTCCTGGCCA 1097
                                                                                                                                                                          TCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTTCCTGGCAA 418
                                                                                                                                                                                                                                                                                                                               TGGCCGTGGCCGACTTGTCGTGCGTGCTGGTCCTGCCCACCCGCCTGGTCTACCACTTCT 977
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                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGGCTTTTCATCCGAGACCACAAGTCCGGGACCCCGGCCAACGTGTTCCTGATGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTCGCCTCCTTCTACCTTCTGGATTTTATCCTGGCTTAGTTGGCAATACCCTGGCTC 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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48.8%;
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Pred. No. 8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1901;
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RESULT 9
PCT-US93-11153-43
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PCT-U893-11153-43
                                                                                                      TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Applicat
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OP INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                      PEATURE
                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                        TELEPHONE: (312) 474-6300
                                                                                                                                                                                                       TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                                             NAME: Noland, Greta E. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole,
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233
                 NAME/KEY: CDS
LOCATION: 701
                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTCCTGTGGGTGGTGGCTGTGGCCATGGCCCCGCTGCTGGTGAGCCCACAGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                 701..1717
                                                                                            linear
                                                                       DNA (genomic)
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RESULT 10 PCT-US95-07180-1

Sequence 1, Application PC/TUS9507180
GENERAL INFORMATION:
APPLICANT: LI, YI

APPLICANT: LI, YI
APPLICANT: GOCAYNE,
APPLICANT: RUBEN, ST
TITLE OF INVENTION:

STEVEN M

JEANINE D

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARREST .

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

STREET: 6 BECK CITY: ROSELAND STATE: NJ

COUNTRY: U: ZIP: 07068

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Best Local Similarity
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                                                                                                                                                                      GTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGG 718
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TOGTGCCTACCACGTCAACCGCTCCGTCTACGTG 1477
                                   TCCTGCCCTATCACACACTGAGGACCGTCCACTTG
                                                                                                         TTTCTCACAGGAAGGCACTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTT 778
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Pred. No. 8e~21;
0; Mismatches 341
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; LOCATION:
PCT-US95-07180-1
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PILING DATE: 06-JUNE-1993

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201994-1700
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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TOPOLOGY: lir
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Similarity 48.8%;
39; Conservative
                                                              GCTACCTGCTGATCATCCGCAGCCTGCGGCAGGCCTGCGTGTGGAGAAGCGCCTCAAG-
                                                                                             GITATCIGCIGATCATICGGGITCIGITAAAAGITGGAGGICCCAGAATCGGGGCIGCGGG 718
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                              TTTCTCACAGGAAGGCACTGACCACCATCATCATCATCATCATCATCTTCTTCTTGTGTT 778
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Pred. No. 9.5e-21;
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US-09-170-496D-181
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CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 181
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Best Local Similarity 48.5%;
Matches 337; Conservative
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Patent No. 65553
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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous,
TITLE OF INVENTION: Receptors
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ORGANISM: Homo
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                                                                                                                                                                     CCATGAACTATATIGCCTIGGTGGTGGGCTGCCTGCCGATTTTTCACACTCAGCATCT
                                                                                                    GITATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGG
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                                                                   GCTACCTGCTGATCATCCGCAGCCTGCGGCAGGGCCTGCGTGTGGAGAAGCGCCTCAAG- 690
                                                                                                                                         CCCTGG-----TGTCCCTGGCAGTGGCCTTCACCTTCCCGTTCATCACCACGGTCACCT
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                               TTTCTCACAGGAAGGCACTGACCACCATCATCACCTTGATCATCTTCTTCTTGTGTT 778
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- ACCAAGGCAAAACGCATGATCGCCATAGTGCTGGCCATCTTCCTGGTCTGCT
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Pred. No. 5.6e-20;
0; Mismatches 343; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/08/097,938
APPLICATION NUMBER: US/08/097,938
PILING DATE: 26-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
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FEATURE:
NAME/KEY:
LOCATION:
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LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SUNDELIN, APPLICANT: SCARBOROU
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                                                                                                                                                                                                                                                                                                         Local Similarity
les 185; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
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446
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                            TTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGG 336
                                                                                                                                                    TTGCCAAGTAACGGCATGGCCCTGTGGGTCTTTCTTTTCCGAACTAAGAIGAAGCACCCT
                                                                                                      GTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCC
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TTGAAGATTGCCTATCACATACATGGCAACAACTGGATTTATGGGGAAGCTCTTTGTAAT 505
                                                                            GCTGTGATTTACATGGCCAATCTGGCCTTGGCTGACCTCCTCTGTCACCTGGTTCCCC
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56..1249
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Pred. No. 1.4e-18
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
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GENERAL INFORMATION:
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Matches 1
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ADLER, REID G.
NAME: 30,988
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SUNDELIN, DULLAN APPLICANT: SCARBOROUGH, ROBERT M.

APPLICANT: SCARBOROUGH, ROBERT M.

APPLICANT: SCARBOROUGH, ROBERT M.

APPLICANT: SCARBOROUGH, ROBERT M.

APPLICANT: SCARBOROUGH, ROBERT M.

APPLICANT: SCARBOROUGH, ROBERT M.

APPLICANT: SUNDELIN, DULLAND RECEPTOR, ITS AGONISTS

TITLE OF INVENTION: NAME ANTAGONISTS, AND NUCLBIC ACIDS ENCODING THE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 25-JAN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                 266 ACTGGAAAACTGACCACTGTCTTCCTTCCAATTGTCTACACAATTGTGTTTTGTGGTGGGT 325
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GTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCC 276
                                                                                                                                                    ATTGAAAACTTCAAGAGAGAATTTTTCCCCAATTGTATATCTGATAATATTTTTCTGGGGA 156
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                                                                         GTCTTGGGAAATGGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCT
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56..1249
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Pred. No. 1.4e-18;
0; Mismatches 155
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US-08-472-840-3
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US-08-472-840-3
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                                         Query Match
Best Local Similarity 54.4%;
Conservative
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                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.,
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APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
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                                                                                                                                                                                         LOCATION:
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CLASSIFICATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                 LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/39
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, RELD G.
REGISTRATION NUMBER: 30,988
REGISTRATION NUMBER: 30,988
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APPLICANT: SCARBOROUGH, ROBERT M.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                              FEATURE:
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Best Local Similarity 98.9%; Matches JOURNAL 181 122 121 62 749; Conservative 61 GGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTT 1 ATGGAGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT 60 N 1 (bases 1 to 758)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)

Contact: Fu GK CD630086 56040032J1 FLP Homo sapi CD630086 CD630086.1 GI:40278352 Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, Tel: 6508454102 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens EST Email: gfu@incyte.com. Homo sapiens (human) TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 240 TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGGAAATGGGTTGTCCATA TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA 180 GGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTT ATGGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT /organism="Homo sapiens" /mol_type="mRNA", /mbl_type="mRNA", /clone_lib="FLP", /note="Vector: pDrive Cloning Vector", Location/Qualifiers FLP Homo sapiens cDNA, mRNA sequence. Score 723; DB 6;] Pred. No. 2.3e-199; 0; Mismatches 5; 758 bp CA 94304, USA mRNA Length 758; Indels linear EST 12-JAN-2004 <u>ω</u> Gaps 121 120 61 181

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Contact: Fu GK
                                                                                                                                                                                    Incyte Genomics, Inc. 3160 Porter Dr., Palo Tel: 6508454102
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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        Conservative
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/mol type="mRNA"
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/note="Vector: pDrive Clo
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1 (bases 1 to 745)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
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Email: gfu@incyte.com
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/db_xref="taxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Cloning Vector"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 726)
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ATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCCATTTTTCACACTCAGCATCTGT
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                                                                  AACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC
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|mol type="mRNA,"
|db_xref="taxon:9606"
|clone_llb="FLP"
|note="Vector: pDrive Cloning Vector"
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBI7 row: f column: 03
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National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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                                                             GAGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCAT
                                                                                                                TATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTT 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malia; Eutheria; (bases 1 to 720)
                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/organism="Homo sapiens"
/ob_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:7389737"
/tissue_type="mixed"
/lab_host="DH108 [T1-phage-resistant)"
/clone_lib="WIH_MGC 146"
/note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pcDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov.image.rearrayed_plates/IRBF.preSV.dat
a. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                     Score 693; DB 7;
Pred. No. 1.3e-190;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                     Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throextension cloning of partial genes Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
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56039988H1 FLP Homo sapiens cDNA,
CD630075
CD630075.1 GI:40278341
                                                                                                                                                                                                                                Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                   gfu@incyte.com
                                                                                  /organism="Homo sapiens"
/mol type="mRNA"
/db xref="teaxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Clo
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Homo sapiens (human)
Homo sapiens
Edwaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 750)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
                                                                                                                                                      CD630077 750
5603999641 FLP Homo sapiens c
CD630077.1 GI:40278343
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Email: gfu@incyte.
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Contact: Fu GK
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3160 Porter Dr., Palo Alto, CA 94304,
Tel: 6508454102
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          729 bp mRNA linear ES
AGENCOURT 30842618 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:7389737 5', mRNA sequence.
C0959148
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 729)
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Homo sapiens
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CO959148.1 GI:51323730
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG
                                                                                           TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGGAAATGGGTTGTCCATA
                                                                                                                                                                           GGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTT
                                                                                                                                                                                                                                    ATGGAGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT
                                                                                                                                                                                                                                                            ATGGAGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT
                                                               TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA
                                                                                                                                                    GGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTT
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="make" | //mol_type="make" | //mol_type="make" | //mol_type="make" | //mol_type="make" | //mol_type="maked" | //clone="IMAGE:7389737" | //tissue_type="mixed" | //lab_host="DH10B (T1-phage-resistant)" | //clone_lib="NIH_MGC_146" | //mote="vector: pcDNA3.1; Site 1: multiple; Site 2: //mote="vector: pcDNA3.1; Site 1: multiple; GRF's were PCR-amplified (from IMAGE Clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pcDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie (website, using the Guthrie ID given in the file ftp://image.llnl.gov_image.rearrayed_plates/IRBF.preSV.data. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                     Score 655.2; DB 7;
Pred. No. 1.4e-179;
0; Mismatches 32;
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Gene

Collection (MGC)

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EST 17-AUG-2004

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> Indels Length 729;

4;

Gaps

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180

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AUTHORS
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                  Best Local Similarity Matches 651; Conserv
                                 Query Match
Best Local (
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                                                                                                                                                                                                 Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA
Tel: 6508454102
                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; 3uteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 652)

Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                            CD630079 652 bp mRNA linea 56040008H1 FLP Homo sapiens cDNA, mRNA sequence. CD630079
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                CD630079.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA
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                 62.5%; Score 651; DB 6; Lv ilarity 100.0%; Pred. No. 2.3e-178; Conservative 0; Mismatches 0;
                                                                                                                                                                                    gfu@incyte.com.
                                                                                  /organism="Homo sapiens"
/mol type="mRNA"
/db xref="ttaxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Cloning
                                                                                                                                                       1. .652
                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                GI:40278345
                                                                                                                                                                                                                94304,
                                           DB 6; Length 652;
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                  Indels
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KEYWORDS
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                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoste Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 670)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
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                                                                                                             Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                         CD630087 670
56040088H1 FLP Homo sapiens
CD630087 CD630087.1 GI:40278353
                                                                              Email: gfu@incyte.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
                                                                         1. .670
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RESULT 12
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           Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 663)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
                                                                                                                                              56040016H1 FLP Homo
CD630081
CD630081.1 GI:40278
                                                                                                           Homo sapiens (human)
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Tel: 6508454102
Email: gfu@incyte
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                                                                                                                                           <u>임</u>
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  sapiens (human)
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
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1 (bases 1 to 682)
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                   GTTATCTGCTGATCATTCGGG 679
                                                                              CCATGAACTATATTGCCTTGGTGGTGGGCCTGCCTGCCATTTTTCACACTCAGCATCT
                                                                                                                      AACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAAATTGCCTAAGCTGCAGA
                                                                                                                                          AACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAA--TTGCTAAGCTGCAGA 598
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 GITATCTGCTGATCATTCCGG
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/mol_type="mRNA"
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/clone_lib="FLP"
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RESULT 14
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: IRBI02 row: f column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
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National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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CF147785.1 GI:33244053
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  GCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA 300
                                                                                                                                                  TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA 180
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                                                                   TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTG
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                                           TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG
                                                                                                                            TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA
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/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
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/clone="IMAGE:6971946"
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/lab_host="DH10B"
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100.0%; Pred. No. 3e-167;
tive 0; Mismatches 0;
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                                                                                                                        1 ATGGAGAGAAATTTAIGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAAACGAAAT
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD630066 633 bp mRNA linea 56039816R6 FLP Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                         Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
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                                                     ATGAACTATATTG 613
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TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA
               TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA 180
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                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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γ	181 TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 240
망	182 TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 241
β	241 GCCATTTCAGAATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA 300
Db	242 GCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA 301
γQ	301 GGCTCCAATTGGATATTTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC 360
Db	302 GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC 361
γQ	361 AACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATG 420
Вb	362 AACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATG 421
Qy	421 GTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG 480
дb	422 GTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG 481
γ	481 ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG 540
Db	482 ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG 541
8	541 AACGGCAGTGTCACATGCTTAGAGC-TGAATCTCTATAAAATTGCTAAGCTGCAGAC 599
DЬ	542 AACGGCAGTGTCACATCATGCTTAGAGCTTGAATCTCTATAAATTGCTAAGCTGCAGAC 601
γ	600 CAT 602
Db	602 CAT 604

Search completed: March Job time: 4057.5 secs 20, 2005, 02:52:32

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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 3, Appli	Seguence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 9, Appli	Sequence 373, App	Sequence 3, Appli	Sequence 15, Appl	2, 7	Sequence 17, Appl	Sequence 206, App

ALIGNMENTS

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APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585,876
CURENT APPLICATION NUMBER: 60/182,061
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRSUSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 346
TYPEE: PRT
CORGANISM: Homo sapiens
US-09-585-876-2
                                                                                                                                                                                                                                                                                                                                                           Query Match 99.5
Best Local Similarity 99.4
Matches 328; Conservative
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                                      FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA
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99.4%;
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US-09-044-404A-2
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FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,79:
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-7:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 610-270-5219
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Patent No.
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APPLICANT:
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MEDIUM TYPE: Diskett.
COMPUTER: IBM Compat.
OPERATING SYSTEM: DO
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APPLICANT: SARAU, HENRY
TITLE OF INVENTION: CDNA CLONE HMI
TITLE OF INVENTION: A MOVEL HUMAN
NUMBER OF SEQUENCES: 2
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TYPE: amino acid
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                                                       190 HYVSLEVGEIIPEVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSEM 247
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PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACENPLLYYEAGENEKDRLK 301
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ELLIS, CATHERINE
AMES, ROBERT
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22, 1997
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CURRENT APPLICATION NUMBER: US/09/586,924
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/844,795
PRIOR FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-586-924-2
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Sequence 44, Application US/08153848 Patent No. 5759804 GENERAL INFORMATION:
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APPLICANT: SATHE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR FILE REFERENCE: GH-70001-1D1
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                                                                                                                                                              302 SALRK 306
                                                                                                                                                                                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                                                           129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
                                                                                                                                                                                                                                                                                                                                                                                                               10 SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
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5. 6506878
                                                                                                                            STFRK 311
                                                                                                                                                                                             PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDFLLYFFSGGNFRKRL-
                                                                                                                                                                                                                                                                                                  NYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
                                                                                                                                                                                                                                                                                                                                      QNINLVTQKKARFVCVGİWİFVİLTSSPFLMAKPQKDGKNNTKCFEPPQDNQTKNHVLVL 189
                                                                                                                                                                                                                             PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
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HALSEY, WENDY
ELLIS, CATHERINE E
AMES, ROBERT S.
FOLEY, JAMES J.
SARAU, HENRY M.
CHAMBERS, JOHN OF OUR
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APPLICANT: APPLICANT: APPLICANT:

Godiska, Ronald Gray, Patrick W. Schweikart, Vicki

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APPLICATION: 514
CILASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
PILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1474-6300
                                                                                       RESULT 5
US-08-812-871-3
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Sequence 3, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 28.0%; Score 479; DB 1; Length 339; Best Local Similarity 34.8%; Pred. No. 1.2e-29; Matches 112; Conservative 62; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
LENGTH: 339 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
                                                                                                                                                                                306 HALCNLLCGKRLKGPPPSFEGK 327
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  RESULT 6
US-09-299-843A-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: pe
IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: 992700
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SOFTWARE: Fast SEQ for Windows Version
CURRENT APPLICATION DATA:
PILICATION NUMBER: US/08/812,871
FILICA PAPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
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APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: SIR
TOPOLOGY: linear
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STATE: CA
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                                                                                         306
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                                                                                                                                                                                                                                                                                                                                                                                                                                            75 VADLSCYLVLPTRLYYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
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                                                                                         HALCNLLCGKRLKGPPPSFEGK 327
                                                                                                                                                                                                                     LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                     MNYIALVVGCLLPFFTLSICYLLIIRVLLKVBVPESGLRVSHR----KALTTIIITLIIFF
                                                                                                                                                                                                                                                                                                                                                        HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMLA
                                                                                                                                                                            VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 amino acids
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Best Local Similarity
Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill B. Uhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
LENGTH: 339 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UW-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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     246
                                       242
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                                                                         192 HALVSLAVAFTFPFITTVTCYLLIIRSL-----ROGLRVEKRLKTKAVRMIAIVLAIFL 245
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                                   LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
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                                                                                                         MNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHR---KALTTIITLIIFF 241
                                                                                                                                                                                       HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV
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                                                                                                                                                                                                                                                                                                                                               FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR
                                                                                                                                                     HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
                                                                                                                                                                                                                                                                                                           FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA
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6300 Sears Tower,
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                                                                                                                                                                                                                                                                                                                                                                                                         28.0%; Score 479; DB 3; Length 339; 34.8%; Pred. No. 1.2e-29;
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US-09-088-337B-44
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.0%; Score 479; DB 3; Length 339; Best Local Similarity 34.8%; Pred. No. 1.2e-29;
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                                                                                                                                                                                                                                                                                                                                                           Matches
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INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy disk
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Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
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MMYIALVVGCLLPFFTLSICYLLIRVLLXVEVPESGLRVSHR---KALTTIIITLIIFF 241
                                                                      HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH
                                                                                                                  HPFRLLHVTSIRSAWILCGIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                                       FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74
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TELEFAX: (312) 474-0448
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PILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 198-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-170-496D-32
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PCT-U893-11153-44
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                                                                                Sequence 44, Application PC/TUS9311153
GENERAL INFORMATION:
GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GE
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Best Local Similarity
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APPLICANT: Chalmors, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
ADDRESSEE: Bicknell
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                             Gerstein,
                                                                                                           Transmembrane Receptors
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PCT-US95-07180-2
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PCT-US93-11153-44
                                                                                Sequence 2, Application PC/TUS9507180
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: COCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                          NUMBER OF SEQUENCES: S
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
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MEDIUM TYPE: Floppy disk
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CITY: C
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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3: Illinois
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CARELLA,
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  BYRNE, BAIN, GILFILLAN, CECCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/977,452
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245

ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD

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US-09-170-496D-182
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Best Local Similarity
                 APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC compatible
COMPUTER: PC COMPATION
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
CLASSIFICATION:
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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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ZIP: 07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version SEQ ID NO 182 LENGTH: 339
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Best Local Similarity
                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/:
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
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APPLICANT:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                   STREET: 130 W
               APPLICATION NUMBER: JP 7-093989 FILING DATE: 19-AUG-1995
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ZIP: 02109
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o. 6114139
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Ohtaki, Tetsuya
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                                                                                        PCT/JP95/01599
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APPLICATION NUMBER:

JP 7-057186

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RESULT 13
US-09-745-842-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PILING DATE: 11-AUG-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 26.9%;
Local Similarity 30.7%;
les 98; Conservative 81
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FILING DATE: 30-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                   141 GVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGIGVRRNKTIT-CYDTTADEY 199
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                                                                                                                                                                                                                       174
                                                                                                                                                                                                                                                                                    123
                                                                                                                                                       234 IITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANACFNPL 287
                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                              63 NLAISDLIFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
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                                                                                                                                                                                                                                                                                                                                                                               GWAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMF
                                                                                          LYYFAGENFKDRLKSALRK 306
                                                                                                                                                                                                                  LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLKVSHRKALTTI
                                                                                                                                                                                                                                                                                 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE-----
                                                                                                                                                                                                                                                                                                                NLALADELYVLTLPALIFYYENKTDWIEGDVMCKLQRFIFHVNLYGSILELTCISVHRYT 140
                                                                                                                                                                                        LRSYFVYSMCTTVFMFCI----PFIVILGCYGLIVKALIYKDLDNSPLR---RKSTYLV
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                                                              LYFLAGDTFRRRLSRATRK 330
                                                                                                                           IIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDFI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 461; DB 3
Pred. No. 3e-28;
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RESULT 14
US-08-559-524A-4
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                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LL
STREET: 1800 M Street, N.M.
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SEQ ID NO 14
LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                       sequence 4, Application US/08559524A
Patent No. 5871963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Ramakrishnan-DuBridge, V
APPLICANT: Julius, David
APPLICANT: Hollopeter, Gunter
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: P2712 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 44481-5053-US
CURRENT APPLICATION NUMBER: US/09/745,842
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 60/171,622
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Homo sapiens
FEATURE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                          COUNTRY: USA
ZIP: 20036-5869
                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVYPLKSLGRLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTIT-CYDTTSDEYL
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Ramakrishnan-DuBridge, Vanitha
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                                                                                                                                                                                                                                                                     RECEPTOR
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US-08-749-707-4
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                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08749707 Patent No. 6063582 GENERAL INFORMATION:
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Matches
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 0444
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 202-467-7000
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                              APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Wichael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                               COUNTRY:
                                                                                                                                                     STATE: D.C
                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                        STREET:
                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 --TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVIIVLTVFAVSYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 IRSAWILCGIIWILIMASSIMLĻ---DSGSEQNGSVTSCLE----LNLYKIAKLQTMN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 PALIFYYENKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLK 164
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                                                                                                                   20036-5869
APPLICATION DATA:
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1800 M Street, N.W.
                                                                                                                                     USA
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; MOLECULE TYPE: protein
US-08-749-707-4
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FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-01-US
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336 SRATRK 341
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Search completed: March 18, 2005, 16:22:31 Job time: 32.7544 secs

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lymplocyte-specifi
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MIP-1 alpha recept
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$33733

$33733

G protein-coupled receptor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: $33733

R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock

FEBS Lett. 324, 219-225, 1993

A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.

A;Reference number: $33733; MUID:93285340; PMID:8508924

A;Accession: $33733

A;Status: preliminary

A;Molecule type: mRUN

A;Residues: 1-362 cWEB>

A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g39508

C;Keywords: G protein-coupled receptor; transmembrane protein
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
356	356	356.5	356.5	356.5	357	360	361.5	363	364.5	366	366	370	370.5	371.5	372
20.8	20.8	20.8	20.8	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.4	21.6	21.6	21.7	21.7
363	359	378	361	333	328	432	352	359	362	427	355	365	383	365	363
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
A49092	A48857	A45680	JC5653	165989	JC4800	A43448	A43113	S15403	JN0694	S17148	G02436	S68679	S55594	S68208	I57940
angiotensin II rec	angiotensin II rec	G protein-coupled	G protein-coupled	G protein-coupled	P2Y6 receptor - hu	thrombin receptor	chemokine (C-C) re	angiotensin II rec	angiotensin II rec	alpha-thrombin rec	chemokine (C-C) re	G protein-coupled	G protein-coupled	G protein-coupled	somatostatin recep

ALIGNMENTS

RESULT 2 150241 G protein N;Alterna C;Species	Db Qy	dg Qy	B S	B 8	g Sy	B 8	Query M Best Lo Matches
RESULT 2 150241 G protein-coupled receptor 6H1 - chicken N;Alternate names: purinoceptor 6H1 C;Species: Gallus gallus (chicken)	288 LYYFAGENFKDRLKSALRK 306 : : : 312 LYFLAGDTFRRLSRATRK 330	234 IITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPL 287 : : : : : : :	174 INLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTI 233	123 AMVHPFRILHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLE 173	63 NLAISDLLEISTLPERADYYLRGSNWIEGDLACRIMSYSLYVNMYSSIYELTVLSVVRFL 122 :: :: :: :: : :	5 GTESNNNSRNCTIENFKREFEPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML 62 : : : : :	Query Match 27.3%; Score 467; DB 2; Length 362; Best Local Similarity 30.7%; Pred. No. 8.7e-31; Matches 98; Conservative 83; Mismatches 112; Indels 26; Gaps 7;

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RESULT 3
1074737
G protein-coupled receptor P2Y1 - human
N; Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C; Species: Homo sapiens (man)
C; Date: 10-May-1996 #sequence revision 16-Aug-1996 #text_change 09-Jul-
C; Accession: JC4737; JC4615; S54253
R; Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.;
Blochem. Blophys. Res. Commun. 221, 588-593, 1996
A; Title: Cloning and tissue distribution of the human P2Y1 receptor.
A; Reference number: JC4737; MUID:96205320; PMID:8630005
A; Accession: JC4737; MUID:96205320; PMID:8630005
                                   A; Molecule type: DNA
A; Residues: 1-373 < JAN>
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C;Keywords: G protein-coupled receptor; transmembrane |
F;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
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F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>
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A;Residues: 1-308 <KAP>
A;Residues: 1-308 <KAP>
A;Coss-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: p2Y5
C; Superfamily: ATP receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L06109; NID:g304183; PIDN:AAB06587.1; A;Experimental source: T-cells C;Comment: This receptor plays a role in T-cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 13-Sep-1996 #seque
C;Accession: I50241; JC461
R;Kaplan, M.H.; Smith, D.I
J. Immunol. 151, 628-636,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Identification of a G protein coupled receptor induced A;Reference number: I50241; MUID:93329058; PMID:8393036 A;Accession: I50241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQNNTEQRTCFE-NFPESTWKTYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 LHVTSIRSAWILCGIIWILIMASSI---MLLDSGSEQNGSVTSCLELNLYKIAKLQTWNY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 SRNCTIE-NFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAL---VVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF 244
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              UNIPROT: P47900;
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36, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 447;
Pred. No. 3.
           GB:S81950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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.2e-29;
       NID:g1839438;
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                                                                                                                                                                                                      #text_change 09-Jul-2004
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    PIDN:AAB47091.1; PID:g18394
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3
                                                                                                              RESULT 4
JC4162
  C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
                                                                                    P2Y receptor -
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Elliot,
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F;11,27,113,197/Binding site: carbohydrate (Asn) (F;258,336/Binding site: phosphate (Ser) (covalent) F;330,339/Binding site: phosphate (Thr) (covalent) F;343/Binding site: phosphate (Thr) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #:52-77/Domain: transmembrane #status predicted <TM1> F:58-111/Domain: transmembrane #status predicted <TM2> F:124-152/Domain: transmembrane #status predicted <TM3> F:171-191/Domain: transmembrane #status predicted <TM3> F:271-291/Domain: transmembrane #status predicted <TM6> F:2614-237/Domain: transmembrane #status predicted <TM6> F:2614-237/Domain: transmembrane #status predicted <TM6> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM7> F:261-282/Domain: transmembrane #status predicted <TM8-282/Domain: transmembrane #status predicted <TM8-282/Domain: transmembrane #status predicted <TM8-282/Domain: transm
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A; Residues: 1-137,139-373 < LEO>
A; Cross-references: EMBL: Z49205;
C; Comment: This receptor belongs
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 3pter-3qter C; Superfamily: ATP receptor P2u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-373 < AYY>
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A;Title: Cloning and chromosomal localization of the human P2Y1 puri A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615
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A;Experimental source: erythro leukemia cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 MVHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE-----L 174
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                                                                                                                  YYFAGENFKDRLKSALRK 306
                                                                                                                                                                                                                                           IVLTVFAVSYIPFHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
                                                                                                                                                                                                                                                                                                                                                              ITLIIFFLCFLPYHTLRTVHLTT----WKVGLC--KDRLHKALVITLALAAANACFNPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSYFIYSMCT----TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR----RKSIYLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVYPLKSLGRLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTIT-CYDTTSDEYL
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9; Mismatches
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Smith,

G.M.

Webb,

T.E.; Dainty, I.A.

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B45680

G protein-coupled peptide receptor EBI 2 - human

G sprotein-coupled peptide receptor EBI 2 - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: B45680

R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-con
A;Reference number: A45680; MUID:93188173; PMID:8383238

A;Accession: B45680

A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: preliminary
A;Cross-references: UNIPROT:B32249; GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIP:127097)

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein
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A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: MRNA
A; Rolecule type: UNIPROT: P48042; EMBL: X87628; NID: g1032484; PID)
A; Experimental source: aortic endothelial cell
C; Genetics:
A; Genetics:
A; Gene: bovp2y
C; Superfamily: ATP receptor P2u
C; Keywords: glycoprotein; phosphoprotein; receptor; transmembrane
C; Keywords: glycoprotein; phosphoprotein; redicted <TM1>
F; 88-11/Domain: transmembrane #status predicted <TM1>
F; 88-11/Domain: transmembrane #status predicted <TM1>
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F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM7>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status F;258/Binding site: phosphate (Ser) (covalent) (by protein kinass A)
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A,Title: Cloning and characterisation of a bovine P2Y receptor.
A,Reference number: JC4162; MUID:95352058; PMID:7626079
A,Recession: JC4162
    Query Match
Best Local Similarity
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    25.7%;
32.1%;
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    Score 440;
Pred. No. 1
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    ; DB 2;
1.4e-28;
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                    Length 361;
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A; Cross-references: UNI
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    FKDRLK 301
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C;Accession: T09508
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2Y5 is encoded in A;Reference number: Z16705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intron 17 purinergic receptor P2Y5 - N;Alternate names: G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                              130 LLHVTSIRSAWILCGIIWILIM---ASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTMN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 NSRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 25.5%; Score 436; DB 2; Length 34. Similarity 32.0%; Pred. No. 2.8e-28; 98; Conservative 73; Mismatches 113; Indels
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                                                                                                                      RÍVIFIEIVĠFFIPLILNVTĆSSMVLKTĹTK-PVTLSRSKINKTKVLKMIFVHLIIFCFĆ
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FVPYN----INLILYSLVRTQTFVNCSVVAAVRTMYPITLCIAVSNCCFDPIVYYFTSDT
                                                       FLPYHTLRTVHLTTWKVGLCKDRLHKALV-----ITLALAAANACFNPLLYYFAGEN
                                                                                                                                                                                                                                                                                                                                                                             LEVETLEERI-EYETTRIWEEGDLLCKISVMLEYTNMYGSILELTCISVDRELAIVYEEK
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A;Cross-references: UNIPROT:P35383; GB:L14751; NID:g309457; PIDN:AAA39871.1; C;Superfamily: ATP receptor P2u C;Keywords: transmembrane protein
                    S
                                                                                                                                                                                                    C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-373 < LUS>
                                                                                                                                                                                      A;Status: preliminary
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C;Superfamily: ATP receptor P2u
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A; Residues: 1-370 < JAN>
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C;Species: Homo sapiens (man)
C;Date: 02-Sep_1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
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                                                  Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                      ;Species: Mus musculus (house mouse);Date: 13-Jan-1995 #text_change;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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Best Local Similarity
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MEP----NGTFSNNN-SRNCTI-ENFKREFFFIVYLIIFFWGVLGNGLSIYVFLQPYKK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLCFLPYHTLRTVHLTTWKVGLCK---DRLHKALV-ITLALAAANACFNPLLYYFAGENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLSQIGTNKKKVLKMITVHMAVF
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ilarity 31.8%;
Conservative 6
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31.7%;
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                                             Score 418.5; DB 2;
Pred. No. 8.2e-27;
7; Mismatches 131;
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Pred. No. 9.3e-28;
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                                               10;
                                                                                                                                     PID:g309458
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RESULT 10
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C;Accession: S13638
C;Accession: S13638
R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, Nature 349, 342-346, 1991
A;Title: Cloning by functional expression of platelet-activating factor receptor A;Reference number: S13638; MUID:91101726; PMID:1846231
A;Accession: S13638
A;Accession: S13638
A;Accession: S13638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-342 <HON>
PID:g
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S13638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              platelet-activating factor receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
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                                                                                                                                                                                                                                LQTMNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF
                                             DRIKSALRKGHPQKAKTKC
                                                                                                                                        LCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPLLYYFAGENFK
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                                                                                          ICFVPHHMVQ-LPWTLAELGMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFR
                                                                                                                                                                                        PVLIIHICIVLGFFIVFLLILFCNLVIIHTLLRQPVKQQRNAEVRRALWMVCTVLAVFV
                                                                                                                                                                                                                                                                                     KTAQATTRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNKAGSGNITRCFB-HYEKGSK
                                                                                                                                                                                                                                                                                                                                   RLLHVTSIRSAWILCGIIWILIM--ASSIMLLD-----SGSEQNGSVTSCLELNLYKIAK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
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-NIMRSSOKC
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receptor

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platelet-activating factor receptor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Catcesion: 28-Aug-1992 #text change 39-Jul-2004
C;Catcesion: A40191; JH0479; Ā41079; JC1359; A42831; I51923
R;Kunz, D; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A;Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, c.
A;Reference numbor: A40191; MUID:92250505; PMID:1374385
A;Accession: A40191; MUID:92250505; PMID:1374385
A;Accession: A40191
A;Molecule type: mRNA
A;Residues: 1-342 <KUN>
A;Cross-references: UNIPROT:P25105; GB:M76674; NID:9456293; PIDN:AAA60002.1; PID:
A;Cross-references: UNIPROT:P25105; GB:M76674; NID:9456293; PIDN:AAA60002.1; PID:
A;Reference numbor: JH0479; MUID:92028922; PMID:1656963
A;Reference numbor: JH0479; MUID:92028922; PMID:1656963
A;Accession: JH0479; MUID:92028922; PMID:1656963
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A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cy. A;Roccession: A54946; MUID:94211846; PMID:8159738

A;Roccession: A54946

A;Status: preliminary
A;Molecule recommendary
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A40191
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C; Date: 11-Nov-1994 #sec
C; Accession: A54946
C; Accession: Sullivan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GDB:362713; OMIM:600041
A,Map position: 11q13.5-11q14.1
C,Buperfamily: ATP receptor P2u
C,Keywords: G protein-coupled receptor; tra
A,Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; A;Experimental source: granulocyte, cell line HL-60 all R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.
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                                                                 A; Molecule type: mRNA
A; Residues: 1-342 < YER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U07225
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A; Residues: 1-375 < PAR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGVLRPLRSLRWGRARYARRVAGAVWVLVLACQAPVLYFVTTSARGPLTCHDTSAPELFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FHLAVSDALYAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILPLTCISVHRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQTMNYIALVVGCL--LPFFTLSICYLLIIRVLLKVEVPES-GLRVSHRKALTTIIITLI
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                                                                                                                                                          functional receptor for plate:
H.; Minami, M.; Bito,
                                          PID:g189538
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A;Residues: 1-226, Trg', 229-342 <SEY>
A;Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698
A;Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R;Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir: Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for an A;Reference number: I51923; MUID:93192035; PMID:8383507
A;Accession: I51923
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R;Sugimoto, T.; Tsuchimochi, H.; McGregor, C.C.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A;Title: Molecular cloning and characterization of the platelet-activating factor receptors, R;Reference number: JC1359; MUID:93112021; PMID:1281995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: the authors translated the codon AAT for residue 316 R;Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992 A;Title: The human platelet-activating factor receptor gene (A;Reference number: A42831; MUID:92347886; PMID:1322356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-315,'N',317-342 <SUG>
A;Experimental source: heart
A;Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;134-155/Domain: transmembrane #status predicted <TIV>F;184-205/Domain: transmembrane #status predicted <TRV>F;233-253/Domain: transmembrane #status predicted <TVI>F;237-297/Domain: transmembrane #status predicted <VII>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: G protein-coupled receptor; transmembrane protein F;17-38/Domain: transmembrane #status predicted <TRI>F;54-75/Domain: transmembrane #status predicted <TII>F;54-75/Domain: transmembrane #status predicted <TII>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 1p35-1p34.3
C;Superfamily: ATP receptor P2u
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A;Molecule type: DNA
A;Residues: 1-342 < RES>
A;Cross-references: GB:S56396; NID:g298580; PIDN:AA
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233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 23.9%;
Similarity 31.3%;
MVCTVLAVFIICFVPHHVVQ-LPWTLAELGFQDSKFHQAINDAHQVTLCLLSTNCVLDPV
                                                                                                                                                                                          LELNIYKIAKLQTMNY IALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALT
                                                                                                                                                                                                                                                                    NRFQAVTRPIKTAQANTRKRGISLSLVIWVAIVGAASYFLILDSTNTVPDSAGSGNVTRC
                                                                                                                                                                                                                                                                                                                                   VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDS-----GSEQNGSVTSC 171
                                                                                                                                                                                                                                                                                                                                                                                                      IFMVNĹTMADMĹFLITĹÞĹWIVYYQNQGNWILPKFLCNVAGCLFFINTYCSVAFLGVITY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
                                                               TIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPL
                                                                                                                           FE-HYEKGSVPVLIIHIFIVFSFFLVFLIILFCNLVIIRTLLMQPVQQQRNAEVKRALW
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platelet activating factor receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Ju C;Accession: S63666 R;Ishii, S:; Matsuda, Y:; Nakamura, M:; Waga, I:; Kume, K:; Izumi, T. Biochem. J. 314, 671-678, 1996 Biochem. J. 314, 671-678, 1996 A;Title: A murine platelet-activating factor receptor gene: cloning, A;Reference number: S63666; MUID:96239129; PMID:8670084
                    S
                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-341 <ISH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Thrombin receptor's specificity for agonist peptide is A;Reference number: I51667; MUID:94195429; PMID:8145852 A;Accession: I51667 A;Accession: I51667 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Gerszten, R.E.; Chen, J
Nature 368, 648-651, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombin receptor - African clawed frog
C;SpecLes: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51667
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Best Local S
Matches 99
                                                                                                                             ;Cross-references: UNIPROT:Q62035; EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g125;Superfamily: ATP receptor F2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: UNIPROT:P47749; EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g4951
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                                                                                           Query Match
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                                                                           Similarity
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MEPNGTFSNNNSRNCTIENFKREFFPIYYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTMNYIALVVGCLL----PFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IADVFFVSVLPFKIAYHLSGNDWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.6%; ilarity 32.4%; Conservative 6
                                                        23.6%;
ilarity 30.5%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                          66;
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Pred. No. 1.3e-
61; Mismatches
                                                    Score 404; DB 2;
Pred. No. 1.1e-25;
6; Mismatches 134
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                                                                                                                                                                                                                                                                                           I.; Kume, K.; Izumi, T.; Shimizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                        134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123;
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                                                                                        Length 341;
                                                        Indels
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A;Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:g1008084; PIDN:CAA90290.1; R;Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, Biochem. J. 314, 1009-1016, 1996
A;Title: Molecular cloning, expression and potential functions of the human prot A;Reference number: S64709; MUID:96177879; PMID:8615752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Eur. J. Biochem. 232, 84-89, 1995
A;Title: Molecular cloning and functional expression of the A;Reference number: 866518; MUID:96048032; PMID:7556175
A;Accession: S66518
                                                                                                                                                                                                     C/Superfamily: ATP receptor P2u F;1-56/Domain: activation peptide #status predicted <APT>F;1-25/Domain: signal sequence #status predicted <SIG>F;37-397/Product: proteinase-activated receptor 2 #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729 A;Note: the authors translated the codon GTC for residue 68 as Ile and AAC for K,KAhn, M.L.; Coughlin, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,'A',139-397 <BOE>
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                                                                                                                                                                                                                                                                                                                   A; Introns: 28/1
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                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: H00822
A; Accession: G02131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-397 < NYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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Best Local :
                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                           29-397
                                                                                                                                 Similarity
FLPÍVÝTÍVFVVGLPSNGMALWVFLFRTKKKHPAVIYMANLALADLLSVIWFPLKIAYHI 136
                                              FFPIVYLIIFFWGVLGNGLSIYVFLQFYKKSTSVNVFMLNLAISDLLFISTLFFRADYYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFMVNLTMADLLFLITLPLWIVYYYNEGDWILPNFLCNVAGCLFFINTYCSVAFLGVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVIYCFLTKKFRKHLS---EKFYSMRSSRKC
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                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                EMBL: U36753;
                                                                                                23.4%; Score 400.5; DB 2; 30.7%; Pred. No. 2.6e-25; tive 69; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                             NID:g1208539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       September 1995
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2 #status predicted
                                                                                                     Indels
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                                                                                                  33;
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A.; Kahn,
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RGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILC 143

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <RES>
A;Cross-references: UNIPROT:P35414; EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g4253
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiotensin receptor homolog APJ - human (Bpccles: Homo sapiens (man) (C;Bpccles: Homo sapiens (man) (C;Datc: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004 (C;Datc: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Datc: 13-4315 (C;Dat
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A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                  239 ---GLR-KRRILISIIVVLVVTFALCMMPYHLVKTLYMLGSLLHWP---CDFDLFLMNIF 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189
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                                                                                                                                            292 PYCTCISYVNSCLNPFLYAFFDPRFRQACTSMLCCGQSRCAGT 334
                                                                                                                                                                                                             274 --TLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKT 314
                                                                                                                                                                                                                                                                                                                                                              218 PESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVH----LTTWKVGLCKDRLHKALVI 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 CLELNLYKIAKLQT------MNYIALVVGCLLPFFTLSICYLLIIRVLI,------KVEV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 TVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWIL--IMASSIMLL-DSGSEQNGSVTS 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRSADIFIASLAVADLTEVVTLPLWATYTYRDYDWEFGTFFCKLSSYLIEVNMYASVFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 STSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEPNGTFSN----NNSRNCTIENFKRE--FFPIVYLIIFFWGVLGNGLSIY-VFLQPYKK 53
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ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM RESULT 1 CO959137/c LOCUS FEATURES COMMENT DEFINITION KEYWORDS VERSION ACCESSION TITLE JOURNAL source Email: cgapbs-r@mail.nih.gov Tissue Procurement: Guthrie cDNA Resource Center cDNA Library Preparation: Guthrie cDNA Resource Center cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: IRBI7 row: f column: 03 CO959137 720 bp mRNA linear EST 17-AUG-2004 AGENCOURT 30842218 NIH MGC 146 Homo sapiens cDNA clone IMAGE:7389737 3', mRNA sequence. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) TSI Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens CO959137.1 GI:51323719 CO959137 Homo sapiens Contact: Daniela S. Gerhard, Ph.D. Mammalia; Eutheria; 1 (bases 1 to 720) e: IRBI7 row: f column: 03 quality sequence start: 20 quality sequence stop: 632. Location/Qualifiers /organisme"Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /db_xref="taxon:9606" /clone="IMAGE:7389737" /tlssue_type="mixed" /lab_host="BH10B (T1-phage-resistant)" /clone_lib="NIH_MGC 146" /clone_lib="NIH_MGC 146" /note="Vector: pcDNA3.1; Site 1: multiple; Site 2: /note="Vector: pcDNA3.1; Site 1: multiple; (human) Euteleostomi; Homo. pe b or

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hon
1 (bases 1 to 758)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throuextension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
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                                                                                                           Homo sapiens (human)
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a. Note: this is a NIH_MGC Library."
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Pred. No. 3e-190;
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Incyte Genomics,
3160 Porter Dr.,
Tel: 6508454102
Email: gfu@incyte
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Similarity 98.9%;
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Location/Qualifiers
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/mol_type="mRNA"
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/clone_lib="FLP"
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                               Homo sapiens cDNA,
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Pred. No. 5.4e-185;
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 762)
Fu.G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
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/note="Vector: pDrive Cloning Vector"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 745)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
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CD630072.1 GI:40278338
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                     GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCT
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/mol type="mRNA"

/mb_xref="taxon:9606"

/clome_llb="FLP"

/note="Vector: pDrive Cloning Vector"
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1 (bases 1 to 726)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD630089 726 bp
56040096H1 FLP Homo sapiens cDNA,
CD630089 GI:40278355
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: gfu@incyte.com
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                                       TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGT
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/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive C
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Eukaryota; Metazoa; Chordata; Craniata; Vert Mammalia; Eutheria; Primates; Catarrhini; Ho 1 (Dases 1 to 753)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Circular rapid amplification of cDNA ends fo extension cloning of partial genes Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
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3160 Porter Dr., Palo Alto,
Tel: 6508454102
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ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gfu@incyte.com.
                                                                                                                                                                                                                                                                                                                                                                                                                         "mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                      Score 632; DB 6; I
Pred. No. 1.8e-172;
0; Mismatches 5;
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AUTHORS
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Matches 683; Conserv
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                                                       \vdash
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Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Pu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56039996H1 FLP Homo sapiens cDNA, CD630077
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD630077.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT
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AAGAGAGAATTTTTCCCCAATTGTATATCTGATAATATTTTTCTGGGGAGCCTTGGGAAAT 120
                                           ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAACTGAAAAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGGGCTGCGGGTTTCTC---ACAGGAAGGCACTGACCACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTCAGCATCTGTTATCTG-CTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATTAAAATTGC
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                           ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC
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                                                                                    Conservative
                                                                                                                                                                                                                                                     gfu@incyte.com
                                                                                                                                               /organism="Homo sapiens"
/mol type="mannA"
/db_xref="raxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:40278343
                                                                                            62.4%;
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                                                                                Score 619.2; DB 6;
Pred. No. 9.8e-169;
0; Mismatches 13;
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CD630069
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                                                                                                                                                               Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)
Contact: Pu GK
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 673)
                                                                                                                                                                                                                                                                                                                       CD630069 673 bp
56039916H1 FLP Homo sapiens cDNA,
CD630069 GI:40278335
                                                                                          Email: gfu@incyte.com.
Location/Qualifiers
                                                                                                                         Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                   1. .673
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/mol type="mRNA"

/db_xref="taxon:9606"

/clone lib="FLP"

/note="Vector: pDrive Cloning Vector"
                                                                                                                                         S
                                                                                                                                         94304,
                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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Best Local Similarity
Matches 618; Conserv
Rukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 729)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbe r@mail.nih.gov

Tissue Procurement: Guthrie cDNA Resource Center

cDNA Library Preparation: Guthrie cDNA Resource Center
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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Plate: IRBI7 row: f
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Similarity 94.7%;
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Location/Qualifiers
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/lab host="DHIOB (T1-phage-resistant)"
/clome_lib="NHIOB (T1-phage-resistant)"
/clome_lib="NHIOB (T46"
/clome_lib="NHIOB (T46"
/note="Vector: pcNN3.1.; Site_1: multiple; Site_2:
/note="Vector: pcN3.1.; Site_1: multiple; Site_2:
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/note="Vector: pcN3.1.; Site_1: multiple; Site_2:
/the Guthrie cDNA pesource Center (www.guthrie.org/cDNA)
/into pcDNA3.1. For specific information on cloning sites
/which vary by clone), please refer to the Guthrie
/website, using the Guthrie ID given in the file
ftp://image.lnl.gov.lmage.rearrayed_plates/IRBF.preSV.dat
a. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7389737"
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1 (bases 1 to 652)

Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
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56040008H1 FLP Homo sapiens cDNA,
CD630079
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3160 Porter Dr., Palo Alto,
Tel: 6508454102
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                              ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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                                                                        TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gfu@incyte.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Clo
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Fu.G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: gfu@incyte.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Fu GK
Incyte Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Similarity 99.7%;
11; Conservative
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TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
                                                                      TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGT
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/mol type="mRNA"

/db_xref="taxon:9606"

/clone lib="FLP"

/note="Vector: pDrive Cloning Vector"
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Pred. No. 5.5e-163;
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Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                 3160 Porter Dr., Palo Alto, Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 663)
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             TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT
                                                          ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC
                                                                                                    GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
                                                                                                                                              AAGAGAGAATTTTTCCCAAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAAT
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/mol type="mRNA"
/db xref="taxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Clo."
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Pred. No. 3.2e-162;
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56039908H1
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CD630067.1
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: gfu@incyte.com
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                        AAGAGAGAATTTTTCCCAATTGTATATATCTGATAATATTTTTCTGGGGAGTCTTTGGGAAAT
ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC
                                                                                      GGGTTGTCCATATATGTTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
                                                                                                                                                 AAGAGAAATTTTTCCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAAT
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                                                              GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
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                                                                                                                                                                                                                                                                                                                 Conservative
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                           Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 729)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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CF147785.1
                                                                                                                                                                                http://image.llnl.gov
Plate: IRBI02 row: f column: 05
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                                                                                                                                                                      quality sequence stop: 659.
                                                      /organism="Homo sapiens"
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/clone="MAGE:6971946"
/tissue_type="mixed"
/lab_hoste"DH108"
/clone lib="NIH MGC 145"
/clone lib="NIH MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORPs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                                                                                                                                                      Location/Qualifiers
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Similarity
                           GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCT
                                                                                                                                     ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCT
                                                                                                       ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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Contact: Fu GK Incyte Genomics, 3160 Porter Dr., Homo sapiens (human) GI:40278332 FLP Homo sapiens Inc. Palo Alto, Chordata; Primates; 633 bp ens cDNA, δ Craniata; Vertebrata; Catarrhini; Hominidae; mRNA sequence. USA Euteleostomi; EST 12-JAN-2004

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Search completed: March 20, Job time: 3872.5 secs
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Matches 554; Conserva
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Location/Qualifiers
                                                  TAAGCTGCAGACCAT 604
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                                                                    TAAGCTGCAGACCAT 554
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/db_xref="taxon:9606"
/clome_llb="FLP"
/note="Vector: pDrive Cloning Vector"
            2005, 02:52:30
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 1, 2005, 11:53:02; Search time 44 Seconds (without alignments) 721.626 Million cell updates/sec

Title: Perfect score: Sequence: US-09-826-791A-2 1712 1 MEPNGTFSNNNSRNCTIENF......KAKTKCVFPVSVWLRKETRV 330

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters: Searched: 283416 seqs, 96216763 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95% Maximum Match 100% Listing first 80 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult No.

Query Score Match Length DB Ħ Description

No matches found

Search completed: April 1, 2005, 12:01:38 Job time : 44 secs

